AMENDMENTS TO THE CLAIMS:

This listing of the claims below will replace all prior versions and listing of claims:

Listing of Claims

194. (Previously presented) A method for identifying a compound that potentially elicits or modulates T1R2/T1R3 (sweet) receptor-associated taste comprising:

(i) screening one or more compounds in a binding assay which identifies compounds that specifically bind to a T1R2/T1R3 (sweet) taste receptor or which specifically modulate (enhance or inhibit) the specific binding of another compound to a T1R2/T1R3 (sweet) taste receptor; and

(ii) identifying compounds that potentially elicit or modulate T1R2/T1R3 (sweet) taste based on their (a) specific binding to a T1R2/T1R3 sweet taste receptor or (b) modulation of the specific binding of said another compound to a T1R2/T1R3 sweet taste receptor.

195. (Previously presented) The method of claim 194 wherein said T1R2 receptor is selected from the group consisting of rat T1R2, mouse T1R2 and human T1R2 and said T1R3 is selected from the group consisting of rat T1R3, mouse T1R3 and human T1R3.

196. (Previously presented) The method of claim 194 wherein said T1R2 and T1R3 are of the same species origin.

197. (Previously presented) The method of claim 194 wherein said T1R2 and T1R3 are of different species origin.

198. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 having the amino acid sequence of SEQ. ID. NO: 6.

199. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 that exhibits at least 90% sequence identity to the polypeptide of SEQ. ID. NO: 6.

200. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 that exhibits at least 95% sequence identity to the polypeptide of SEQ. ID. NO: 6.

201. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 that exhibits at least 96% sequence identity to the polypeptide of SEQ. ID. NO: 6.

202. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 that exhibits at least 97% sequence identity to the polypeptide of SEQ. ID. NO: 6.

203. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 that exhibits at least 98% sequence identity to the polypeptide of SEQ. ID. NO: 6.

204. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 that exhibits at least 99% sequence identity to the polypeptide of SEQ. ID. NO: 6.

205. (Previously presented) The method of claim 194 wherein said T1R2 is encoded by the nucleic acid sequence of SEQ. ID. NO: 10.

206. (Previously presented) The method of claim 194 wherein said T1R2 is encoded by a nucleic acid sequence that hybridizes to the nucleic acid sequence of SEQ. ID. NO: 10 under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, and 1% SDS and washing at 65°C in a solution comprising 0.2X SSC and 0.1% SDS.

207. (Previously presented) The method of claim 194 wherein said T1R2 is a fragment of the polypeptide encoded by the nucleic acid sequence of SEQ ID. NO: 10 that when expressed in association with a T1R3 polypeptide yields a T1R2/T1R3 sweet taste receptor that specifically binds to sweet taste stimuli.

208. (Previously presented) The method of claim 194 wherein said T1R2 is a fragment of the human T1R2 polypeptide of SEQ. ID. NO. 6 that when expressed in association with a T1R3 polypeptide results in a heteromeric T1R2/T1R3 taste receptor that specifically binds sweet taste stimuli.

209. (Previously presented) The method of claim 194 wherein said T1R3 is a human T1R3 having the amino acid sequence of SEQ. ID. NO: 7.

210. (Previously presented) The method of claim 194, wherein said T1R3 polypeptide possesses at least 90% sequence identity to the polypeptide of SEQ. ID. NO: 7.

211. (Previously presented) The method of claim 194, wherein said T1R3 polypeptide possesses at least 95% sequence identity to the polypeptide of SEQ. ID. NO: 7.

212. (Previously presented) The method of claim 194, wherein said T1R3 polypeptide possesses at least 96% sequence identity to the polypeptide of SEQ. ID. NO: 7.

213. (Previously presented) The method of claim 194, wherein said T1R3 polypeptide possesses at least 97% sequence identity to the polypeptide of SEQ. ID. NO: 7.

214. (Previously presented) The method of claim 194, wherein said T1R3 polypeptide possesses at least 98% sequence identity to the polypeptide of SEQ. ID. NO: 7.

215. (Previously presented) The method of claim 194, wherein said T1R3 polypeptide possesses at least 99% sequence identity to the polypeptide of SEQ. ID. NO: 7.

216. (Withdrawn) The method of claim 194 wherein the T1R3 polypeptide is a rat T1R3 polypeptide having the sequence contained in SEQ. ID. NO: 4.

217. (Previously presented) The method of claim 194 wherein the T1R3 polypeptide is encoded by the nucleic acid sequence of SEQ ID. NO: 9.

218. (Currently amended) The method of claim 194 wherein said T1R3 polypeptide is encoded by a nucleic acid sequence that hybridizes to the nucleic acid sequence of SEQ. ID. NO: 9 under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, and 1% SDS and washing at 65°C in a solution comprising 0.2X SSC and 0.1% SDS~~or fragments thereof that encodes a T1R3 polypeptide that when expressed in association with a T1R2 polypeptide yields a heteromeric umani T1R2/T1R3 taste receptor that specifically binds umani taste stimuli~~.

219. (Previously presented) The method of claim 194 wherein said T1R2/T1R3 receptor is expressed by a cell.

220. (Previously presented) The method of claim 194 wherein said T1R2/T1R3 receptor is present in a membrane extract.

221. (Previously presented) The method of claim 194 wherein said T1R2/T1R3 receptor is attached to a solid phase.

222. (Previously presented) The method of claim 194 wherein said T1R2/T1R3 receptor is in solution.

223. (Previously presented) The method of claim 194 wherein said T1R2/T1R3 receptor is present in a lipid bilayer or vesicle.

224. (Previously presented) The method of claim 219 wherein said cell is an intact or permeabilized cell.

225. (Previously presented) The method of claim 219 wherein said cell further expresses a G protein.

226. (Previously presented) The method of claim 219 wherein said cell is a prokaryotic cell.

227. (Previously presented) The method of claim 219 wherein said cell is an eukaryotic cell.

228. (Previously presented) The method of claim 227 wherein said cell is an insect, yeast, amphibian or mammalian cell.

229. (Previously presented) The method of claim 227 wherein said cell is a CHO cell, HEK-293 cell, COS cell or Xenopus oocyte.

230. (Previously presented) The method of claim 194 wherein the binding assay detects changes in the conformation of the T1R2/T1R3 heteromeric receptor.

231. (Previously presented) The method of claim 230 wherein said changes are detected by NMR spectroscopy.

232. (Previously presented) The method of claim 230 wherein said changes are detected by fluorescence spectroscopy.

233. (Previously presented) The method of claim 194 wherein said T1R2/T1R3 (sweet) taste receptor further comprises a G protein.

234. (Previously presented) The method of claim 230 wherein said G protein is $G_{\alpha 15}$, $G_{\alpha 16}$ or gustducin.

235. (Previously presented) The method of claim 194 wherein said binding assay includes the use of a detectable label.

236. (Previously presented) The method of claim 235 wherein said label is an enzyme, radio nuclide, chemiluminescent compound or fluorescent compound.

237. (Previously presented) The method of claim 197 wherein the binding assay detects displacement of a labeled ligand from said T1R2/T1R3 heteromeric receptor.

238. (Previously presented) The method of claim 194 wherein said binding assay is a fluorescence polarization or FRET assay.

239. (Previously presented) The method of claim 194 wherein the binding assay detects conformational changes in the T1R2/T1R3 taste receptor based on altered susceptibility to proteolysis.

240. (Previously presented) The method of claim 194 wherein the binding assay is a competitive binding assay.

241. (Previously presented) The method of claim 194 wherein the binding assay is a non-competitive binding assay.

242. (Previously presented) The method of claim 194 wherein the binding assay detects the specific binding of said compound to said receptor.

243. (Previously presented) The method of claim 194 wherein said binding assay detects the binding of a natural or artificial sweetener compound to said receptor.

244. (Previously presented) The method of claim 194 wherein said binding assay uses a cell that stably expresses the T1R2/T1R3 receptor on its surface.

245. (Previously presented) The method of claim 194 wherein said binding assay uses a cell that transiently expresses the T1R2/T1R3 receptor on its surface.

246. (Previously presented) The method of claim 194 wherein the binding assay uses an HEK-293 cell that stably expresses T1R2/T1R3 and further expresses $G_{\alpha 15}$.

247. (Previously presented) The method of claim 246 wherein said binding assay detects the effect of said compound on the binding of a radioactively or fluorescently labeled ligand to said receptor.

248. (Previously presented) The method of claim 194 wherein said binding assay detects binding based on a detectable change in fluorescence absorbance or refractive index.

249. (Previously presented) The method of claim 194 wherein the binding assay is a high-throughput screening assay.

250. (Previously presented) The method of claim 247 wherein the assay screens a combinatorial chemical library.

251. (Previously presented) The method of claim 247 wherein the assay screens a randomized small compound library.

252. (Previously presented) The method of claim 194 which further includes step (iii) wherein the effect of said compound on a T1R2/T1R3 (sweet) taste receptor is confirmed in a human or animal taste test.

253. (New) The method of claim 219, wherein the cell is an endogenous taste cell.

254. (New) The method of claim 253, wherein the cell is a taste cell present in foliate, circumvallate or fungiform papillae.

255. (New) The method of claim 253, wherein the cell is a taste cell present in geschmackstreifen, oral cavity, gastrointestinal epithelium or epiglottis.

256. (New) The method of claim 255, wherein the cell is a taste cell present in gastrointestinal epithelium.

257. (New) The method of claim 194,

wherein said T1R2 comprises a chimeric T1R2 polypeptide which contains a region which is at least 90% identical to either the extracellular or transmembrane region of an endogenous human T1R2 polypeptide and further contains the extracellular or transmembrane region of a different G protein coupled receptor (GPCR); or

wherein said T1R3 comprises a chimeric T1R3 polypeptide which contains a region which is at least 90% identical to either the extracellular or transmembrane region of an endogenous human T1R3 polypeptide and further contains the extracellular or transmembrane region of a different G protein coupled receptor (GPCR).

258. (New) The method of claim 257, wherein said endogenous human T1R2 polypeptide has the amino acid sequence of SEQ. ID. NO: 6.

259. (New) The method of claim 257, wherein said endogenous human T1R2 polypeptide exhibits at least 90% sequence identity to the polypeptide of SEQ. ID. NO: 6.

260. (New) The method of claim 257, wherein said endogenous human T1R2 polypeptide exhibits at least 95% sequence identity to the polypeptide of SEQ. ID. NO: 6.

261. (New) The method of claim 257, wherein said endogenous human T1R2 polypeptide is encoded by the nucleic acid sequence of SEQ. ID. NO: 10.

262. (New) The method of claim 257, wherein said endogenous human T1R2 polypeptide is encoded by a nucleic acid sequence that hybridizes to the nucleic acid sequence of SEQ. ID. NO: 10 under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, and 1% SDS and washing at 65°C in a solution comprising 0.2X SSC and 0.1% SDS.

263. (New) The method of claim 257, wherein said endogenous human T1R2 polypeptide is a fragment of the polypeptide encoded by the nucleic acid sequence of SEQ ID. NO: 10 that when expressed in association with a T1R3 polypeptide yields a T1R2/T1R3 sweet taste receptor that specifically binds to sweet taste stimuli.

264. (New) The method of claim 257, wherein said endogenous human T1R2 polypeptide is a fragment of the human T1R2 polypeptide of SEQ. ID. NO. 6 that when expressed in association

with a T1R3 polypeptide results in a heteromeric T1R2/T1R3 taste receptor that specifically binds sweet taste stimuli.

265. (New) The method of claim 257, wherein said endogenous human T1R3 polypeptide has the amino acid sequence of SEQ. ID. NO: 7.

266. (New) The method of claim 257, wherein said endogenous human T1R3 polypeptide exhibits at least 90% sequence identity to the polypeptide of SEQ. ID. NO: 7.

267. (New) The method of claim 257, wherein said endogenous human T1R3 polypeptide exhibits at least 95% sequence identity to the polypeptide of SEQ. ID. NO: 7.

268. (New) The method of claim 257, wherein said endogenous human T1R3 polypeptide is encoded by the nucleic acid sequence of SEQ ID. NO: 9.

269. (New) The method of claim 257, wherein said endogenous human T1R3 polypeptide is encoded by a nucleic acid sequence that hybridizes to the nucleic acid sequence of SEQ. ID. NO: 9 under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, and 1% SDS and washing at 65°C in a solution comprising 0.2X SSC and 0.1% SDS.

270. (New) The method of claim 257, wherein said endogenous human T1R3 polypeptide is a fragment of the polypeptide encoded by the nucleic acid sequence of SEQ ID. NO: 9 that when expressed in association with a T1R2 polypeptide yields a T1R2/T1R3 sweet taste receptor that specifically binds to sweet taste stimuli.

271. (New) The method of claim 257, wherein said endogenous human T1R3 polypeptide is a fragment of the human T1R3 polypeptide of SEQ. ID. NO. 7 that when expressed in association with a T1R2 polypeptide results in a heteromeric T1R2/T1R3 taste receptor that specifically binds sweet taste stimuli.

272. (New) A method for identifying a compound that potentially elicits or modulates a T1R2/T1R3 (sweet) receptor-associated taste comprising:

(i) screening one or more compounds in a binding assay which identifies compounds that specifically bind to a T1R2/T1R3 (sweet) taste receptor or which specifically modulate (enhance or inhibit) the specific binding of another compound to a T1R2/T1R3 (sweet) taste receptor; and

(ii) identifying compounds that potentially elicit or modulate T1R1/T1R3 (sweet) taste based on their (a) specific binding to a T1R2/T1R3 sweet taste receptor or (b) modulation of the specific binding of said another compound to a T1R2/T1R3 sweet taste receptor,

wherein said T1R2 is an endogenous human T1R2 polypeptide and wherein said T1R3 is an endogenous human T1R3 polypeptide.

273. (New) The method of claim 272, wherein said endogenous human T1R2 polypeptide has the amino acid sequence of SEQ. ID. NO: 6.

274. (New) The method of claim 272, wherein said endogenous human T1R2 polypeptide exhibits at least 90% sequence identity to the polypeptide of SEQ. ID. NO: 6.

275. (New) The method of claim 272, wherein said endogenous human T1R2 polypeptide exhibits at least 95% sequence identity to the polypeptide of SEQ. ID. NO: 6.

276. (New) The method of claim 272, wherein said endogenous human T1R2 polypeptide is encoded by the nucleic acid sequence of SEQ. ID. NO: 10.

277. (New) The method of claim 272, wherein said endogenous human T1R2 polypeptide is encoded by a nucleic acid sequence that hybridizes to the nucleic acid sequence of SEQ. ID. NO: 10 under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, and 1% SDS and washing at 65°C in a solution comprising 0.2X SSC and 0.1% SDS.

278. (New) The method of claim 272, wherein said endogenous human T1R2 polypeptide is a fragment of the polypeptide encoded by the nucleic acid sequence of SEQ ID. NO: 10 that when expressed in association with a T1R3 polypeptide yields a T1R2/T1R3 sweet taste receptor that specifically binds to sweet taste stimuli.

279. (New) The method of claim 272, wherein said endogenous human T1R2 polypeptide is a fragment of the human T1R2 polypeptide of SEQ. ID. NO. 6 that when expressed in association

with a T1R3 polypeptide results in a heteromeric T1R2/T1R3 taste receptor that specifically binds sweet taste stimuli.

280. (New) The method of claim 272, wherein said endogenous human T1R3 polypeptide has the amino acid sequence of SEQ. ID. NO: 7.

281. (New) The method of claim 272, wherein said endogenous human T1R3 polypeptide exhibits at least 90% sequence identity to the polypeptide of SEQ. ID. NO: 7.

282. (New) The method of claim 272, wherein said endogenous human T1R3 polypeptide exhibits at least 95% sequence identity to the polypeptide of SEQ. ID. NO: 7.

283. (New) The method of claim 272, wherein said endogenous human T1R3 polypeptide is encoded by the nucleic acid sequence of SEQ ID. NO: 9.

284. (New) The method of claim 272, wherein said endogenous human T1R3 polypeptide is encoded by a nucleic acid sequence that hybridizes to the nucleic acid sequence of SEQ. ID. NO: 9 under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, and 1% SDS and washing at 65°C in a solution comprising 0.2X SSC and 0.1% SDS.

285. (New) The method of claim 272, wherein said endogenous human T1R3 polypeptide is a fragment of the polypeptide encoded by the nucleic acid sequence of SEQ ID. NO: 9 that when expressed in association with a T1R2 polypeptide yields a T1R2/T1R3 sweet taste receptor that specifically binds to sweet taste stimuli.

286. (New) The method of claim 272, wherein said endogenous human T1R3 polypeptide is a fragment of the human T1R3 polypeptide of SEQ. ID. NO. 7 that when expressed in association with a T1R2 polypeptide results in a heteromeric T1R2/T1R3 taste receptor that specifically binds sweet taste stimuli.

287. (New) The method of claim 194, wherein said endogenous human T1R3 polypeptide is a fragment of the polypeptide encoded by the nucleic acid sequence of SEQ ID. NO: 9 that when expressed in association with a T1R2 polypeptide yields a T1R2/T1R3 sweet taste receptor that specifically binds to sweet taste stimuli.

288. (New) The method of claim 194, wherein said endogenous human T1R3 polypeptide is a fragment of the human T1R3 polypeptide of SEQ. ID. NO. 7 that when expressed in association with a T1R2 polypeptide results in a heteromeric T1R2/T1R3 taste receptor that specifically binds sweet taste stimuli.